SEQUENCE LISTING

<110> Chandrashekar, Ramaswamy
Morales, Tony H.

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<211> 271
<212> PRT
<213> Dirofilaria immitis

<400> 9

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Met Phe Leu Tyr Gly Lys Leu Ile Arg Pro Leu Val Leu Val Leu Glu
 1               5                  10                  15

Val Ser Glu Met Thr Thr Ala Phe Gln Thr Gln Val Val Pro Met Pro
            20                  25                  30

Val Cys Arg Tyr Glu Ile Leu Glu Gly Gly Pro Thr Gly Ala Pro Val
        35                  40                  45

Arg Phe Ala Met Ile Gly Asp His Val Tyr His Lys Trp Thr Cys Asp
    50                  55                  60

Ser Glu Thr Thr Asp Thr Phe Cys Ala Leu Val His Ser Cys Val Val
65                  70                  75                  80

Asp Asp Gly Lys Gly Asp Ala Val Glu Ile Leu Asn Glu Glu Gly Cys
                85                  90                  95

Ala Leu Asp Lys Tyr Leu Leu Asn Asn Leu Glu Tyr Ile Thr Asp Leu
            100                 105                 110

Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala Asp Arg Ser Glu
        115                 120                 125

Leu Tyr Tyr Gln Cys Gln Ile Ser Ile Thr Ile Lys Glu Pro His Ser
    130                 135                 140

Glu Cys Pro Arg Pro Gln Cys Thr Glu Pro Gln Gly Phe Gly Ala Ile
145                 150                 155                 160

Lys Ser Gly Gln Gly Phe Ala Ala Val Lys Ser Ala Ala Ala Pro Ala
                165                 170                 175

Pro Glu Ala Ser Leu Leu Ser Pro Arg Leu Ile Lys Lys Arg Ser Ile
            180                 185                 190

Asn Ser Asp Asn Thr Val Asp Val Ser Thr Gly Phe Ser Thr Val Asp
        195                 200                 205
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Ile Thr Glu Glu Asn Pro Asn Phe Ser Ala Asn Arg Leu Ser Ser Ser
210 215 220

Thr Ser Arg Glu Gln Phe Asn Gly Ile Phe Cys Ile Ala Ser Asn Asp
225 230 235 240

Ile Leu Leu Ile Ile Leu Phe Gly Ala Met Leu Ala Ile Ala Cys Ile
245 250 255

Phe Phe Thr Ala Phe Leu Val His Ser Asn Asn His Ser Lys Ser
260 265 270

<210> 10
<211> 813
<212> DNA
<213> Dirofilaria immitis

<400> 10
tgatttagaa tgattattgg aatgaacaag aaaagcggta aaaaatatgc aagcaatagc 60

taacatagca ccgaacaaaa tgataagtaa aatatcattt gatgcaatac agaagatacc 120

attgaattgt tcacggctcg ttgatgatga taaacgattt gctgagaagt tcggattctc 180

ttcggttata tcaaccgtgc taaaaccggt actgacgtcc accgtattat cagaattaat 240

tgatcgcttc ttgatcaatc gtggagaaag caaggaagct tctggagctg gtgcagcagc 300

agattttaca gcagcaaatc cttgtccaga ttttatggca ccaaatcctt gtggctctgt 360

gcattgtggt cgaggacatt cgctatgtgg ctctttaatt gttatactaa tctggcattg 420

atagtaaagt tctgatcgat ctgcatattt ataaacatga gcttcttggc cagccattaa 480

atctgtaata tattccaaat tattgagtaa atatttgtcc aaagcacatc cttcttcatt 540

cagaatctcc actgcatcac cttttccatc atccacaaca catgaatgta ctaatgcaca 600

gaatgtatct gtagtctctg aatcacatgt ccatttgtga tatacatgat ctccaatcat 660

tgcaaatcga acaggtgcac cagttggtcc accttccaaa atctcatatc gacatacggg 720

cattggtacc acttgagttt ggaatgctgt agtcatttca gatacttcaa ggaccagtac 780

taacggtctt atcagctttc catataaaaa cat 813

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 11
ggctggccaa gaagctcacg tatacaaata tgcg 34

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 12
cgcatatttg tatacgtgag cttcttggcc agcc 34

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13
ggtttaatta cccaagtttg ag 22

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 14
ccatcctaat acgactcact atagggc 27

<210> 15
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 15
ggttatatca accgtgctaa aaccggtact gacgtccacc g 41

<210> 16
<211> 892
<212> DNA
<213> Brugia malayi

<220>
<221> CDS
<222> (158)..(892)

<400> 16
ggtttaatta cccaagtttg agatcattaa aattgatcat caataattca ataatttgtt 60

gcaatttcaa attaatcatt ttgctaattc tattattcca actattttca tcactaatca 120

ctgagaagaa atcaggaaga aagaagcaaa aagttaa atg ttg cat atg caa att 175
Met Leu His Met Gln Ile
1 5

tgc tca ttt ttg tca tat atg ata ata gca agt att aat gct att cca 223
Cys Ser Phe Leu Ser Tyr Met Ile Ile Ala Ser Ile Asn Ala Ile Pro
10 15 20

att gat aat ggt gtc gaa agt gaa cct gaa att gaa tgt ggt cca aca 271
Ile Asp Asn Gly Val Glu Ser Glu Pro Glu Ile Glu Cys Gly Pro Thr
25 30 35

tca atc act gtt aat ttt aat act cga aat cct ttt gaa gga cat gta 319
Ser Ile Thr Val Asn Phe Asn Thr Arg Asn Pro Phe Glu Gly His Val
40 45 50

tat gct aaa gga tta tac agt aat caa gat tgt cgt agt gat gaa ggt 367

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Tyr Ala Lys Gly Leu Tyr Ser Asn Gln Asp Cys Arg Ser Asp Glu Gly
 55                  60                  65                  70

gga cgt cag gta gcc gga ata tca tta ccg ttt gat tca tgt aat gtc   415
Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp Ser Cys Asn Val
                 75                  80                  85

gca cgt aca cgt tcg tta aat cca cgt gga ata ttt gtc aca gct gtt   463
Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe Val Thr Ala Val
             90                  95                 100

gtg gta att acg ttt cat cca cag ttt atc aca aaa gtt gat cga aca   511
Val Val Ile Thr Phe His Pro Gln Phe Ile Thr Lys Val Asp Arg Thr
        105                 110                 115

tat cga ttg caa tgc ttt tac atg gaa gct gat aag act gtt agc aca   559
Tyr Arg Leu Gln Cys Phe Tyr Met Glu Ala Asp Lys Thr Val Ser Thr
    120                 125                 130

caa att gaa gtt tcc gaa atg aca acc gta ttt gct aca caa ttg gta   607
Gln Ile Glu Val Ser Glu Met Thr Thr Val Phe Ala Thr Gln Leu Val
135                 140                 145                 150

cca atg cct gtg tgt aga tat gag att ctg gat ggt ggt cca acc gga   655
Pro Met Pro Val Cys Arg Tyr Glu Ile Leu Asp Gly Gly Pro Thr Gly
                155                 160                 165

caa cct gtc cag tat gct aat att gga caa ccg gtt tat cat aaa tgg   703
Gln Pro Val Gln Tyr Ala Asn Ile Gly Gln Pro Val Tyr His Lys Trp
            170                 175                 180

aca tgt gat tct gaa aca gtt gat acc ttc tgt gct ttg gta cat tcc   751
Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala Leu Val His Ser
        185                 190                 195

tgt ttt gtt gat gat ggc aat ggt gac agt att aat tta att aat gaa   799
Cys Phe Val Asp Asp Gly Asn Gly Asp Ser Ile Asn Leu Ile Asn Glu
    200                 205                 210

gaa gga tgt gca tta gat cga tat ctt cta aat aat ttg gaa tat cca   847
Glu Gly Cys Ala Leu Asp Arg Tyr Leu Leu Asn Asn Leu Glu Tyr Pro
215                 220                 225                 230

act gat cta atg gct ggc caa gaa gct cac gta tac aaa tat gcg       892
Thr Asp Leu Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala
                235                 240                 245
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<210> 17
<211> 245
<212> PRT
<213> Brugia malayi

<400> 17
Met Leu His Met Gln Ile Cys Ser Phe Leu Ser Tyr Met Ile Ile Ala
1 5 10 15

Ser Ile Asn Ala Ile Pro Ile Asp Asn Gly Val Glu Ser Glu Pro Glu
20 25 30

Ile Glu Cys Gly Pro Thr Ser Ile Thr Val Asn Phe Asn Thr Arg Asn
35 40 45

Pro Phe Glu Gly His Val Tyr Ala Lys Gly Leu Tyr Ser Asn Gln Asp
50 55 60

Cys Arg Ser Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro
65 70 75 80

Phe Asp Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly
85 90 95

Ile Phe Val Thr Ala Val Val Val Ile Thr Phe His Pro Gln Phe Ile
100 105 110

Thr Lys Val Asp Arg Thr Tyr Arg Leu Gln Cys Phe Tyr Met Glu Ala
115 120 125

Asp Lys Thr Val Ser Thr Gln Ile Glu Val Ser Glu Met Thr Thr Val
130 135 140

Phe Ala Thr Gln Leu Val Pro Met Pro Val Cys Arg Tyr Glu Ile Leu
145 150 155 160

Asp Gly Gly Pro Thr Gly Gln Pro Val Gln Tyr Ala Asn Ile Gly Gln
165 170 175

Pro Val Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe
180 185 190

Cys Ala Leu Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Ser
195 200 205

Ile Asn Leu Ile Asn Glu Glu Gly Cys Ala Leu Asp Arg Tyr Leu Leu
210 215 220

Asn Asn Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His
225   230   235   240

Val Tyr Lys Tyr Ala
                245

<210> 18
<211> 892
<212> DNA
<213> Brugia malayi

<400> 18
cgcatatttg tatacgtgag cttcttggcc agccattaga tcagttggat attccaaatt 60

atttagaaga tatcgatcta atgcacatcc ttcttcatta attaaattaa tactgtcacc 120

attgccatca tcaacaaaac aggaatgtac caaagcacag aaggtatcaa ctgtttcaga 180

atcacatgtc catttatgat aaaccggttg tccaatatta gcatactgga caggttgtcc 240

ggttggacca ccatccagaa tctcatatct acacacaggc attggtacca attgtgtagc 300

aaatacggtt gtcatttcgg aaacttcaat ttgtgtgcta acagtcttat cagcttccat 360

gtaaaagcat tgcaatcgat atgttcgatc aacttttgtg ataaactgtg gatgaaacgt 420

aattaccaca acagctgtga caaatattcc acgtggattt aacgaacgtg tacgtgcgac 480

attacatgaa tcaaacggta atgatattcc ggctacctga cgtccacctt catcactacg 540

acaatcttga ttactgtata atcctttagc atatacatgt ccttcaaaag gatttcgagt 600

attaaaatta acagtgattg atgttggacc acattcaatt tcaggttcac tttcgacacc 660

attatcaatt ggaatagcat taatacttgc tattatcata tatgacaaaa atgagcaaat 720

ttgcatatgc aacatttaac tttttgcttc tttcttcctg atttcttctc agtgattagt 780

gatgaaaata gttggaataa tagaattagc aaaatgatta atttgaaatt gcaacaaatt 840

attgaattat tgatgatcaa ttttaatgat ctcaaacttg ggtaattaaa cc   892